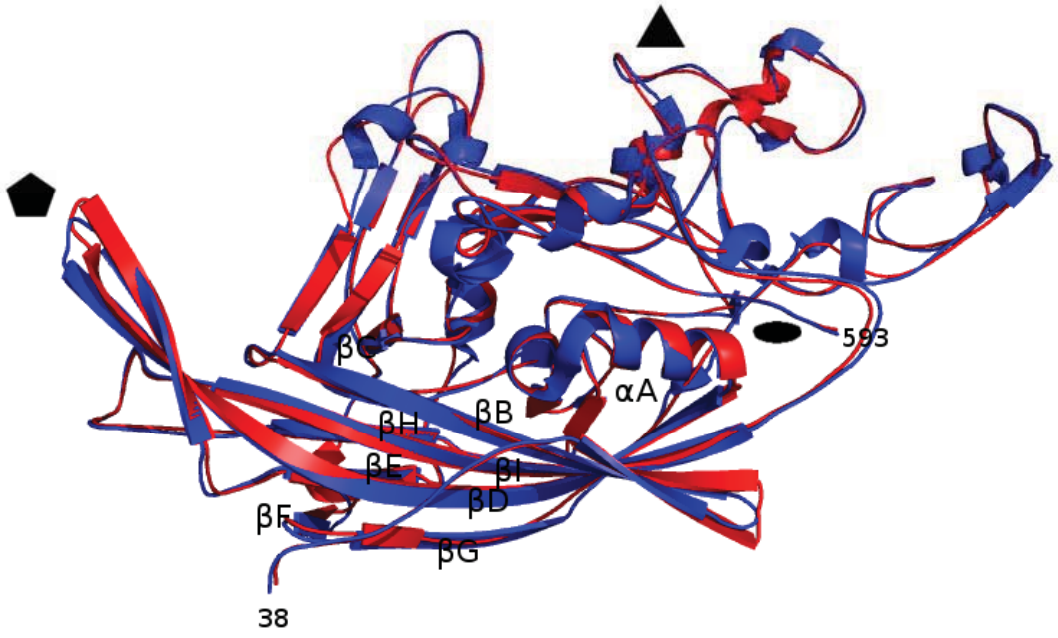
Supplementary Fig. 1. *In silico* model of H-1PV VP2 capsid protein. The ribbon diagrams of H-1PV (red) and MVM (blue) VP2 are superimposed showing the positions of the conserved β-strands, βB to βI, helix αA, and loops regions. The first N-terminal residue (G38 for H-1PV corresponding to G39 for MVM) and the last C-terminus residues (Y592 for H-1PV corresponding to Y587 for MVM) are numbered with reference to the VP1 sequence of which VP2 is an integral part. The approximate position of the icosahedral two-, three-, and fivefold axes are shown as filled oval, triangle, and pentagon, respectively. This figure was generated using the CPHmodels 3.0 Server at the Center for Biological Sequence Analysis of the Technical University of Denmark DTU as described in the Materials and Methods section.

Supplementary Fig. 2. 3D structural alignment of H-1PV and MVM VP2s and identification of potential H-1PV sialic acid binding residues. MVM VP2 from model 1Z14 (pink) and H-1PV VP2 sequence (light blue) were aligned using the "align" routine implemented in the PyMol software. Only the MVM VP2 region 361-369 containing amino acids Ile-362 and Lys-368 (displayed in red) known to bind to sialic acid is represented. The related residues in the H-1PV VP2 sequence 366-374 are Ile-367 and His-373 (displayed in deep blue).



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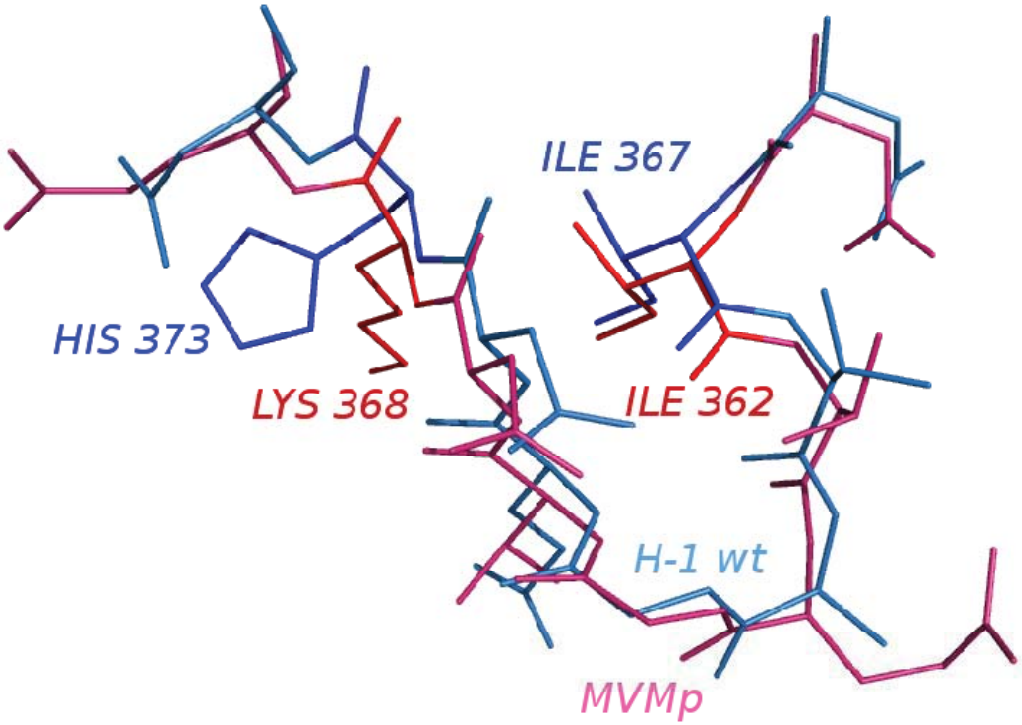

Allaume et al. Suppl. Fig. 2